cell or animal with a polypeptide comprising an amino acid sequence selected from the group consisting of residues 320-673 of SEQ ID NO:2, residues 212-454 of SEQ ID NO:4, SEQ ID NO:6, and residues 213-455 of SEQ ID NO:8 or fragment thereof sufficient to elicit said antibody, whereby the antibody is elicited.

a6 cont

REMARKS

The enclosed specification is identical to the specification of the prior application 09/709,126. The foregoing amendments to the enclosed specification are identical to those made in 09/709,126 except for updating the cross-reference to related applications.

The new claims are directed to the antibody counterparts of the claims issued and allowed in 09/285,502 and 09/709,126, respectively. Claims 14-22 provide comparable limitations to those of claims 14-21 and 25 allowed in 09/709,126. Support for antibodies specific to the extracellular and intracellular domains of KUZ polypeptides is found on p.8, lines 15-17; support for polyclonal antibodies is found on p.8, lines 16-29; support for monoclonal antibodies is found on p.8, line 30 - p.9, line 16; support for single-chain antibodies is found on p.9, lines 17-19; support for KUZ-specific antibody fragments is found on p.9, lines 19-28; support for mouse antibodies is found on p.8, line 24; support for human antibodies is found on p.9, lines 7-11; support for chimeric antibodies is found on p.9, lines 11-15; support for fluorescently labeled antibodies is found on p.8, lines 7-10.

These amendments add no new matter.

The Examiner is invited to call the undersigned if she would like to amend the claims to clarify the foregoing or seeks further clarification of the claim language.

The Commissioner is hereby authorized to charge any fees or credit any overcharges relating to this communication to our Deposit Account No. 19-0750 (order no. B97-081-7).

Respectfully submitted,
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VERSION WITH MARKINGS TO SHOW CHANGES MADE

First paragraph following "BRIEF DESCRIPTION OF THE DRAWINGS" on p.3:

Figure 1 (A). Sequence alignment of predicted KUZ proteins from Drosophila (DKUZ, SEQ ID NO:2), mouse (MKUZ, SEQ ID NO:8) and Xenopus (XKUZ, SEQ ID NO:10). The full length amino acid sequence of MKUZ was deduced from the nucleotide sequence of two overlapping cDNA clones. Partial amino acid sequence of XKUZ was deduced from the nucleotide sequence of a PCR product that includes parts of the disintegrin and Cys-rich domains. The alignments were produced using Geneworks software (IntelliGenetics). Residues identical among two species are highlighted. Predicted functional domains are indicated. Amino acid sequences from which degenerate PCR primers were designed are indicated with arrows. Orthologs of *kuz* are also present in C. elegans (GenBank accession nos. D68061 and M79534), rat (Z48444), bovine (Z21961) and human (Z48579).

Paragraph bridging p.26 and 27:

Xenopus *kuz* was cloned by PCR using degenerate primers (XK1) and (XK4) which correspond to Drosophila KUZ sequence HNFGSPHD (SEQ ID NO:2, residues 609-616) and GYCDVF (SEQ ID NO:2, residues 870-875), respectively. First strand cDNA from stage 18 Xenopus embryos was used as template in a standard PCR reaction with an annealing temperature of 50˚C. A PCR product of expected size was purified and used as template for another PCR reaction using a nested primer (XK3), corresponding to Drosophila KUZ sequence EECDCG (SEQ ID NO:2, residues 688-693), and XK4. The PCR product was subcloned into Bluescript and sequenced. Anti-sense RNA was used as a probe for whole mount *in situ* hybridization of Xenopus embryos according to standard procedures (Harland, R. (1991). Meth. Cell Biol. *36*, 685-695).